OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:52:00 ; Search time 652 Seconds
(without alignments)
6228.252 Million cell updates/sec

Title: US-10-751-612-1
Perfect score: 3016
Sequence: 1 tctagagcataggcattgta.....gggctatgtcaagtccatgg 3016

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5915009 seqs, 673212896 residues

Total number of hits satisfying chosen parameters: 11830018

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	43.4	1.4	4001	7	US-10-517-441-782	Sequence 782, App
	2	43.4	1.4	12963	7	US-10-517-441-655	Sequence 655, App
c	3	42.2	1.4	3201	6	US-10-526-108-278	Sequence 278, App
c	4	42.2	1.4	5649	7	US-10-517-441-569	Sequence 569, App
c	5	41.2	1.4	3201	6	US-10-526-108-260	Sequence 260, App
c	6	41.2	1.4	5649	7	US-10-517-441-295	Sequence 295, App
c	7	40.8	1.4	837	9	US-60-655-875-45247	Sequence 45247, A
	8	40.6	1.3	2240	7	US-10-517-441-542	Sequence 542, App
c	9	40.2	1.3	21561	8	US-11-033-545-641	Sequence 641, App
c	10	40.2	1.3	21561	8	US-11-033-545-797	Sequence 797, App
c	11	40.2	1.3	152768	9	US-60-660-591-42	Sequence 42, Appl
c	12	39.6	1.3	465	9	US-60-655-875-32913	Sequence 32913, A
	13	39.4	1.3	651	9	US-60-655-875-78273	Sequence 78273, A
	14	39.4	1.3	1340	9	US-60-655-875-40651	Sequence 40651, A
	15	39.4	1.3	1397	9	US-60-655-875-59969	Sequence 59969, A
c	16	39.4	1.3	1870	9	US-60-655-875-5998	Sequence 5998, Ap
	17	39.4	1.3	2215	9	US-60-655-875-25420	Sequence 25420, A
c	18	39.4	1.3	2838	9	US-60-655-875-14257	Sequence 14257, A
	19	39.4	1.3	12610	7	US-10-517-441-715	Sequence 715, App
	20	39	1.3	2240	7	US-10-517-441-268	Sequence 268, App
c	21	38.8	1.3	1247	6	US-10-499-065A-123	Sequence 123, App
c	22	38.8	1.3	1785	6	US-10-499-065A-124	Sequence 124, App
c	23	38.8	1.3	2416	6	US-10-499-065A-125	Sequence 125, App
	24	38.8	1.3	2501	6	US-10-526-108-211	Sequence 211, App
	25	38.4	1.3	1622	9	US-60-655-875-15619	Sequence 15619, A
c	26	38.4	1.3	24040	9	US-60-655-875-69	Sequence 69, Appl
c	27	38.2	1.3	1755	9	US-60-655-875-78617	Sequence 78617, A
c	28	38.2	1.3	1836	9	US-60-655-875-14550	Sequence 14550, A
	29	38.2	1.3	2501	6	US-10-526-108-202	Sequence 202, App
	30	38.2	1.3	2501	6	US-10-526-108-212	Sequence 212, App
	31	38.2	1.3	4001	6	US-10-526-108-160	Sequence 160, App
	32	38.2	1.3	4001	6	US-10-526-108-172	Sequence 172, App
c	33	38.2	1.3	4060	9	US-60-655-875-8328	Sequence 8328, Ap
c	34	38	1.3	803	9	US-60-655-875-36665	Sequence 36665, A
c	35	38	1.3	2946	9	US-60-655-875-3469	Sequence 3469, Ap
	36	37.8	1.3	932	9	US-60-655-875-53583	Sequence 53583, A
c	37	37.8	1.3	980	9	US-60-655-875-31184	Sequence 31184, A
c	38	37.8	1.3	1690	9	US-60-655-875-53247	Sequence 53247, A
	39	37.8	1.3	2410	9	US-60-655-875-22583	Sequence 22583, A
	40	37.8	1.3	2990	9	US-60-655-875-471	Sequence 471, App
c	41	37.6	1.2	877	9	US-60-655-875-45203	Sequence 45203, A
c	42	37.6	1.2	1528	9	US-60-655-875-39339	Sequence 39339, A
	43	37.6	1.2	4001	7	US-10-517-441-508	Sequence 508, App
	44	37.6	1.2	9353	7	US-10-517-441-735	Sequence 735, App
	45	37.6	1.2	12963	7	US-10-517-441-381	Sequence 381, App

ALIGNMENTS

RESULT 1
US-10-517-441-782
; Sequence 782, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 782
; LENGTH: 4001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-782

Query Match 1.4%; Score 43.4; DB 7; Length 4001;
Best Local Similarity 52.5%; Pred. No. 0.27;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1219 GAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTT 1278
Db 802 GTGGATTTTTTTTTTTGGGAGGTGGTGGTATTAGTTTAGAGTTTGTATTTTTATTTATTG 861

```
Qy       1279 GAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTC 1338
             | | |    ||   |||  |||  ||   | ||  || ||| |||   | || |    |
Db        862 GGGAAGTGTGGGGAGAAGGATGGGTTGGAGTTGGGTTTTGGTTTGAAGGATAGTAGTTTG 921

Qy       1339 TACATTTAGTTGGTATCATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGA 1398
              | |   | | |  |  | ||  || |||||||  |      || | |   |  |  | ||
Db        922 GAGTTAATGGTTGAGTTTTTAAAGTTTTTATATTGTAGAGGAAGTATAGTGGAGATTAGT 981

Qy       1399 T 1399
              |
Db        982 T 982
```

RESULT 2
US-10-517-441-655
; Sequence 655, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 655
; LENGTH: 12963
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-655

Query Match 1.4%; Score 43.4; DB 7; Length 12963;
Best Local Similarity 52.5%; Pred. No. 0.44;
Matches 95; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

```
Qy       1219 GAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTT 1278
             | ||||  |  ||||  | | ||| | |  | ||||   |  ||||| ||||| || ||
Db        801 GTGGATTTTTTTTTTTGGGAGGTGGTGGTATTAGTTTAGAGTTTGTATTTTTATTTATTG 860

Qy       1279 GAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTC 1338
             | | |    ||   |||  |||  ||   | ||  || ||| |||   | || |    |
Db        861 GGGAAGTGTGGGGAGAAGGATGGGTTGGAGTTGGGTTTTGGTTTGAAGGATAGTAGTTTG 920

Qy       1339 TACATTTAGTTGGTATCATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGA 1398
              | |   | | |  |  | ||  || |||||||  |      || | |   |  |  | ||
Db        921 GAGTTAATGGTTGAGTTTTTAAAGTTTTTATATTGTAGAGGAAGTATAGTGGAGATTAGT 980

Qy       1399 T 1399
              |
Db        981 T 981
```

RESULT 3
US-10-526-108-278/c
; Sequence 278, Application US/10526108
; GENERAL INFORMATION:
; APPLICANT: Maier, Sabine
; TITLE OF INVENTION: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF BREAST CELL PROLIFERA
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 47675-102
; CURRENT APPLICATION NUMBER: US/10/526,108
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2003/007827
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: DE10255104.9
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: DE10239313.3
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 396
; SEQ ID NO 278
; LENGTH: 3201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-526-108-278

Query Match 1.4%; Score 42.2; DB 6; Length 3201;
Best Local Similarity 55.0%; Pred. No. 0.52;
Matches 83; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```
Qy       2023 TAAAAATATAATCTTGAGCTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATAC 2082
             ||| || |   | |    | |||   || | || |   | | |  ||  ||||  |||||
Db        468 TAATAAAAACTTATAACACAAACAAAAAAAACAACAAACACTATAATTAACTCCAAAATAC 409

Qy       2083 ATGATAGATACAATATGAGAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCA 2142
              | ||| | | || |  | | | |||| | |  | ||   || |||  ||||   | | |
Db        408 AAAATAAAAAAAAAAAAAAAAACAAAAAAAAAAACTATTAAATACTCAACATAATACCTA 349

Qy       2143 TACAATATGAGATTTCATCTAAGAGCCAACA 2173
              | ||||  | |||  ||  || |  || ||
Db        348 AATAATAAAATATTCTATACAACAAACACCA 318
```

RESULT 4
US-10-517-441-569/c
; Sequence 569, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147

; SEQ ID NO 569
; LENGTH: 5649
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-569

Query Match 1.4%; Score 42.2; DB 7; Length 5649;
Best Local Similarity 55.0%; Pred. No. 0.66;
Matches 83; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 2023 TAAAAATATAATCTTGAGCTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATAC 2082
Db 3465 TAATAAAAACTTATAACACAAACAAAAAAACAACAAACACTATAATTAACTCCAAAATAC 3406

Qy 2083 ATGATAGATACAATATGAGAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCA 2142
Db 3405 AAAATAAAAAAAAAAAAAAAAACAAAAAAAAAAACTATTAAATACTCAACATAATACCTA 3346

Qy 2143 TACAATATGAGATTTCATCTAAGAGCCAACA 2173
Db 3345 AATAATAAAATATTCTATACAACAAACACCA 3315

RESULT 5
US-10-526-108-260/c
; Sequence 260, Application US/10526108
; GENERAL INFORMATION:
; APPLICANT: Maier, Sabine
; TITLE OF INVENTION: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF BREAST CELL PROLIFER
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 47675-102
; CURRENT APPLICATION NUMBER: US/10/526,108
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/EP2003/007827
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: DE10255104.9
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: DE10239313.3
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 396
; SEQ ID NO 260
; LENGTH: 3201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-526-108-260

Query Match 1.4%; Score 41.2; DB 6; Length 3201;
Best Local Similarity 54.7%; Pred. No. 0.97;
Matches 82; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 2023 TAAAAATATAATCTTGAGCTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATAC 2082
Db 468 TAATAAAAACTTATAACACAAACAAAAAAACAACAAACACTATAATTAACTCCAAAATAC 409

Qy 2083 ATGATAGATACAATATGAGAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCA 2142
Db 408 AAAATAAAAAAAAAAAAAAAAACAAAAAAAAAAACTATTAAATACTCGACATAATACCTA 349

Qy 2143 TACAATATGAGATTTCATCTAAGAGCCAAC 2172
Db 348 AATAATAAAATATTCTATACAACAAACACC 319

RESULT 6
US-10-517-441-295/c
; Sequence 295, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 295
; LENGTH: 5649
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-295

Query Match 1.4%; Score 41.2; DB 7; Length 5649;
Best Local Similarity 54.7%; Pred. No. 1.2;
Matches 82; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 2023 TAAAAATATAATCTTGAGCTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATAC 2082
Db 3465 TAATAAAAACTTATAACACAAACAAAAAAACAACAAACACTATAATTAACTCCAAAATAC 3406

Qy 2083 ATGATAGATACAATATGAGAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCA 2142
Db 3405 AAAATAAAAAAAAAAAAAAAAACAAAAAAAAAAACTATTAAATACTCGACATAATACCTA 3346

Qy 2143 TACAATATGAGATTTCATCTAAGAGCCAAC 2172
Db 3345 AATAATAAAATATTCTATACAACAAACACC 3316

RESULT 7
US-60-655-875-45247/c
; Sequence 45247, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 45247
; LENGTH: 837
; TYPE: DNA

```
;   ORGANISM: Heterodera glycines
US-60-655-875-45247

  Query Match             1.4%;  Score 40.8;  DB 9;  Length 837;
  Best Local Similarity   50.0%;  Pred. No. 0.71;
  Matches  102;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy       1223 ATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTTGAGC 1282
              ||||   |||| | |    |||   ||  || |||||||    |||| | |     |
Db        461 ATGAACTTTTTTTAGAAAAAATTTAATGCATTTTTAAATTAATTTTTTGGGTTCAAAATA 402

Qy       1283 ATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTCTACA 1342
              |||    |||    | | ||||||   | |||   | |   |      | |    | ||
Db        401 ATGTTTTTCTTCTTTTTTAATTTAATTTATATAAAGACAAATTGAAAAATTAATTTTAAT 342

Qy       1343 TTTAGTTGGTATCATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGATGCT 1402
              |||| ||  |||    || | || |   || |||  | | |||  | ||  |  |||  |
Db        341 TTTATTTTTTATTGCTAAAAATAATGCGTTTTCAATTGACTTTATTTAAAATATGATTTT 282

Qy       1403 TTGACTCTTCAAGATTCTTGGAAT 1426
              ||   | ||  | ||  ||  | |
Db        281 TTTTATATTTTAAATGTTTTTATT 258


RESULT 8
US-10-517-441-542
; Sequence 542, Application US/10517441
; GENERAL INFORMATION:
;  APPLICANT: FOEKENS, John
;  APPLICANT:  HARBECK, Nadia
;  APPLICANT:  KOENIG, Thomas
;  APPLICANT:  MAIER, Sabine
;  APPLICANT:  MARTENS, John
;  APPLICANT:  MODEL, Fabian
;  APPLICANT:  NIMMRICH, Inko
;  APPLICANT:  RUJAN, Tamas
;  APPLICANT:  SCHMITT, Armin
;  APPLICANT:  SCHMITT, Manfred
;  APPLICANT:  LOOK, Maxime P.
;  APPLICANT:  MARX, Almuth
;  APPLICANT:  HOEFLER, Heinz
;  TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
;  TITLE OF INVENTION:  proliferative disorders
;  FILE REFERENCE: 47675-93
;  CURRENT APPLICATION NUMBER: US/10/517,441
;  CURRENT FILING DATE:  2004-12-11
;  PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: DE 10317955.0
;  PRIOR FILING DATE: 2003-04-17
;  PRIOR APPLICATION NUMBER: DE 10300096.8
;  PRIOR FILING DATE: 2003-01-07
;  PRIOR APPLICATION NUMBER: DE 10245779.4
;  PRIOR FILING DATE: 2002-10-01
;  NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 542
;   LENGTH: 2240
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-542

  Query Match             1.3%;  Score 40.6;  DB 7;  Length 2240;
  Best Local Similarity   48.5%;  Pred. No. 1.2;
  Matches  142;  Conservative    0;  Mismatches  149;  Indels    2;  Gaps    1;

Qy       1098 TATTTGTTCGAAATTTTTTACTCTCACAAAAGCTAGCTTTTATAGACGGGCATAAAAGCT 1157
              |||||  |  ||||||  |   |  ||||     |||     ||  |  ||   |
Db        289 TATTTTATTTTTATTTTTAATAATGGTTAAAGTGTTTGTTTGGTTTTGGTAAGTAAGAGT 348

Qy       1158 ATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATGAATATCATGTCGAACTA 1217
              | |  |  |   | | || || ||||||   ||||     |   | |  | |      ||

Db        349 GTTAATTAAAAATGTAAGTGTATTATTTATAGTATATATATTAGTTTTATTTTTAGTGTA 408

Qy       1218 TGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTT 1277
              |  |||||  |||    || ||  ||        || | |    |  | ||||  ||  |
Db        409 ATGTGTTGATAAATTTTATAAGGTATTTAATATGTTTTTGAGGGTTGATTTTTTTTTAAT 468

Qy       1278 TGAGCATGAAGGTCTGAACTATGAATTTATGATGT--ATTGTGGCTTGTGAGCTACTCCG 1335
              |     | | |  | | |   |||  |||||  | |  ||| |    |  ||   |  |
Db        469 TTTTAAAGTATATTTTATTAATGTTTTTATATTTTTAATTTTTTGTAATGTTTTTTTATT 528

Qy       1336 CTCTACATTTAGTTGGTATCATAAATATTATTATATTATCATATAAATTTGAT 1388
              | || ||||  ||| ||  |||||| || | | ||  |  ||  |||||| |
Db        529 ATTTATATTTGTTTGTTAAGATAAATTTTTTAAAATATTTGTAATAATTTGTT 581


RESULT 9
US-11-033-545-641/c
; Sequence 641, Application US/11033545
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/11/033,545
;  CURRENT FILING DATE:  2005-01-12
;  PRIOR APPLICATION NUMBER: 60/231,401
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 641
;   LENGTH: 21561
;   TYPE: DNA
;   ORGANISM: Human
US-11-033-545-641

  Query Match             1.3%;  Score 40.2;  DB 8;  Length 21561;
  Best Local Similarity   47.8%;  Pred. No. 4;
  Matches  117;  Conservative    0;  Mismatches  128;  Indels    0;  Gaps    0;

Qy       1176 TTTAATATTTAACTTATACCATATGAATATCATGTCGAACTATGAGGATGATACTTTTCT 1235
              ||  || | ||   |||| |||| |  |    |  | |  | | |   || | |
Db       2565 TTATATGTATATTATATATAATATATAATTATGTTATATATTATATGTATATTATATATA 2506

Qy       1236 GAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAA 1295
                | | |||  || |  ||||| ||     || ||  |  |  |  || | | |    |
Db       2505 ATATATAATTATGTTATATATTATATGTATATTATATATAATATATAATTATGTTACATA 2446

Qy       1296 CTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTCTACATTTAGTTGGTATC 1355
              |||   | ||| || |||  |   | | |  |    | ||  | ||| |   |||
Db       2445 TTATATGTATATTATATATAATATATAATTATGTTATATATTATATGTATATTATATATA 2386

Qy       1356 ATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGATGCTTTGACTCTTCAAG 1415
              ||| ||| |  |    ||| |||| || | ||  |    | ||  ||  ||  ||  |
Db       2385 ATATATAATTGTTATATATTATATGTATATTATATATAATATATAATTATACAATTATAT 2326

Qy       1416 ATTCT 1420
              |||  |
Db       2325 ATTAT 2321


RESULT 10
US-11-033-545-797/c
; Sequence 797, Application US/11033545
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000790
;  CURRENT APPLICATION NUMBER: US/11/033,545
;  CURRENT FILING DATE:  2005-01-12
;  PRIOR APPLICATION NUMBER: 60/231,401
```

```
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 10823
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 797
;   LENGTH: 21561
;   TYPE: DNA
;   ORGANISM: Human
US-11-033-545-797

  Query Match             1.3%;  Score 40.2;  DB 8;  Length 21561;
  Best Local Similarity   47.8%;  Pred. No. 4;
  Matches  117;  Conservative    0;  Mismatches  128;  Indels    0;  Gaps    0;

Qy       1176 TTTAATATTTAACTTATACCATATGAATATCATGTCGAACTATGAGGATGATACTTTTCT 1235
             ||  || | ||   |||| |||| |  |    | | |   | |   ||  | |
Db       2565 TTATATGTATATTATATATAATATATAATTATGTTATATATTATATGTATATTATATATA 2506

Qy       1236 GAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAA 1295
              |  | |||  || |  ||||| ||     || ||  |  |  |  || | | |    |
Db       2505 ATATATAATTATGTTATATATTATATGTATATTATATATAATATATAATTATGTTACATA 2446

Qy       1296 CTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTCTACATTTAGTTGGTATC 1355
              |||   | ||| || |||  |   |  | |  |    | ||  | || |   |||
Db       2445 TTATATGTATATTATATATAATATATAATTATGTTATATATTATATGTATATTATATATA 2386

Qy       1356 ATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGATGCTTTGACTCTTCAAG 1415
              ||| ||| |  |    ||| |||| || | ||  |    | ||  ||  ||  ||  |
Db       2385 ATATATAATTGTTATATATTATATGTATATTATATATAATATATAATTATACAATTATAT 2326

Qy       1416 ATTCT 1420
              ||| |
Db       2325 ATTAT 2321


RESULT 11
US-60-660-591-42/c
; Sequence 42, Application US/60660591
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  John Geisler
;  APPLICANT:  Ravi Jain
;  APPLICANT:  Xing-Xian Yu
;  TITLE OF INVENTION: COMPOSITIONS AND THEIR USES DIRECTED TO METABOLISM GENES
;  FILE REFERENCE: DPTK-0073US.L
;  CURRENT APPLICATION NUMBER: US/60/660,591
;  CURRENT FILING DATE:  2005-03-10
;  NUMBER OF SEQ ID NOS: 2263
;  SOFTWARE: PatentSeq version 1.0
; SEQ ID NO 42
;   LENGTH: 152768
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-660-591-42

  Query Match             1.3%;  Score 40.2;  DB 9;  Length 152768;
  Best Local Similarity   47.1%;  Pred. No. 9.2;
  Matches  123;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy       1176 TTTAATATTTAACTTATACCATATGAATATCATGTCGAACTATGAGGATGATACTTTTCT 1235
             | ||   | ||   |||| ||||  | |||    |  ||   |    || ||| | || |
Db      15595 TATATATTATATTATATATCATAATATTATATATTATAATATTATATATCATAATATTAT 15536

Qy       1236 GAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAA 1295
               |    ||  | | |   | || ||| || | |||  | |   |  || |      | |
Db      15535 ATATTATATATCATAATATTATATATTATAATATTATATATCATAATATTATATATTATA 15476

Qy       1296 CTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTCTACATTTAGTTGGTATC 1355
              |||  |  |      |||| |  || | |  |  |      ||  |||  |  |||
Db      15475 ATATTATATATCATAATATTATATATTATAATATTATATATCATAATATTATATATTATA 15416

Qy       1356 ATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGATGCTTTGACTCTTCAAG 1415
              ||| ||  |||   || ||  |||| |||  |  ||  |  ||  |  |  |    |  |
Db      15415 ATATATTATATATCATAATATTATATATTATAATAATATTATATATCATAATATTATATA 15356

Qy       1416 ATTCTTGGAATGACTTATCAT 1436
                |   |   || |  ||||||
Db      15355 TTATATAATATTATATATCAT 15335


RESULT 12
US-60-655-875-32913/c
; Sequence 32913, Application US/60655875
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/60/655,875
;  CURRENT FILING DATE:  2005-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 32913
;   LENGTH: 465
;   TYPE: DNA
;   ORGANISM: Heterodera glycines
US-60-655-875-32913

  Query Match             1.3%;  Score 39.6;  DB 9;  Length 465;
  Best Local Similarity   58.5%;  Pred. No. 1.2;
  Matches   69;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy       1292 TGAACTATGAATTTATGATGTATTGTGGCTTGTGAGCTACTCCGCTCTACATTTAGTTGG 1351
             | || | |  |||||  |||||| | | || | |  |  | |    |||||||| |
Db        213 TAAATTTTACATTTATTTTGTATTTTTGGTTCTAAAATGATTCATATTACATTTAGCTAT 154

Qy       1352 TATCATAAATATTATTATATTATCATATAAATTTGATCAACTTGAGATGCTTTGACTC 1409
              | ||   | | ||||  |   ||   | ||||||||  || ||| ||   |||  | |
Db        153 TTTCGAGATTTTTATGCTTAAATTTAACAAATTTGAAGAATTTGTGAATATTTTGCCC 96


RESULT 13
US-60-655-875-78273
; Sequence 78273, Application US/60655875
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/60/655,875
;  CURRENT FILING DATE:  2005-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 78273
;   LENGTH: 651
;   TYPE: DNA
;   ORGANISM: Heterodera glycines
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (626)..(626)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (635)..(635)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   OTHER INFORMATION: Genomic contig location: Contig_ID=SeqID_14257; Location=48..698;
;   OTHER INFORMATION: Strand=-
;   FEATURE:
;   OTHER INFORMATION: SCN-specific regions: Sequence locations=1-108,257-316,338-362,38
;   OTHER INFORMATION: -403,425-541,628-651
US-60-655-875-78273

  Query Match             1.3%;  Score 39.4;  DB 9;  Length 651;
  Best Local Similarity   53.6%;  Pred. No. 1.5;
  Matches   82;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       2324 TAATTCTAAAATGATGCCAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTA 2383
             |||||  |||||  |   |||||||      |    ||    ||| || | ||| || | |
Db        167 TAATTGCAAAATTTTATAAAATAAAAGAGAAAATAAAGCAAAAAGGAAGAAAATACCCAA 226

Qy       2384 AAATAGGATGGAAAGTTTTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAA 2443
              || || ||||||      |  | || || | |  | |  || ||| ||  |    || ||
Db        227 GAAAAGAATGGAATAAAATTGAAAGAAAAATTGCGAAAAAAATGGGGACATATCGCAAAA 286

Qy       2444 CCAAACATAAAGAGTTAAATGCATGGTAGGCTC 2476
                |   || ||  | | || | || |  |  ||
Db        287 ATATTTATGAATGGATTAAAGAATTGGGGCTTC 319


RESULT 14
US-60-655-875-40651
; Sequence 40651, Application US/60655875
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/60/655,875
;  CURRENT FILING DATE:  2005-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 40651
;   LENGTH: 1340
;   TYPE: DNA
;   ORGANISM: Heterodera glycines
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(18)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (81)..(81)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1294)..(1294)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1308)..(1308)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1316)..(1316)
;   OTHER INFORMATION: n is a, c, g, or t
US-60-655-875-40651

  Query Match             1.3%;  Score 39.4;  DB 9;  Length 1340;
  Best Local Similarity   50.3%;  Pred. No. 2.1;
  Matches   97;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy       2267 AGGTTTATGTTGTGTTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCATCTAA 2326
             ||||||  |    |||||    |||||| | || || ||     |   || || |  | |||
Db        536 AGGTTTTTAAAATGTTTAAAATGCCAAATATTTAATAAAAATAATAAATGTTCACTTTAA 595

Qy       2327 TTCTAAAATGATGCCAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTAAAA 2386
                ||| |  ||    ||  ||  || |   |||| || || ||    |||| | |
Db        596 AGATAATAGTATAGTGAAACAATTTAAACACCAAATTTTAATGATTTAAAACTTTTTGCG 655

Qy       2387 TAGGATGGAAAGTTTTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAACCA 2446
                |  ||  | | |||  || | |   |||   | |  || |     |    |||
Db        656 GATTATAAAGATTTTAATAAAATTCAAATAATTTTTTAGGGTTATACAGCTCCAATTTAT 715

Qy       2447 AACATAAAGAGTT 2459
                | |||| | | ||
Db        716 AGCATAGAAAATT 728


RESULT 15
US-60-655-875-59969
; Sequence 59969, Application US/60655875
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey
;  APPLICANT:  Du, Zijing
;  APPLICANT:  Guo, Liang
;  APPLICANT:  Kovalic, David
;  APPLICANT:  Lu, Maolong
;  APPLICANT:  McCarter, James
;  APPLICANT:  Miller, Nancy
;  APPLICANT:  Williams, Deryck
;  APPLICANT:  Vaudin, Mark
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
;  TITLE OF INVENTION:  IN PLANTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 38-21(53885)
;  CURRENT APPLICATION NUMBER: US/60/655,875
;  CURRENT FILING DATE:  2005-02-24
;  NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 59969
;   LENGTH: 1397
;   TYPE: DNA
;   ORGANISM: Heterodera glycines
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1376)..(1376)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   OTHER INFORMATION: Genomic contig location: Contig_ID=SeqID_5998; Location=151..1547
;   OTHER INFORMATION: Strand=-
;   FEATURE:
;   OTHER INFORMATION: SCN-specific regions: Sequence locations=1-49,71-95,118-136,158
;   OTHER INFORMATION: -274,361-462,568-610,639-665,687-705,854-913,935-959,982-1000,102
;   OTHER INFORMATION: -1278,1300-1397
US-60-655-875-59969

  Query Match             1.3%;  Score 39.4;  DB 9;  Length 1397;
  Best Local Similarity   53.6%;  Pred. No. 2.1;
  Matches   82;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       2324 TAATTCTAAAATGATGCCAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTA 2383
             |||||  |||||  |   |||||||      |    ||    ||| || | ||| || | |
Db        764 TAATTGCAAAATTTTATAAAATAAAAGAGAAAATAAAGCAAAAAGGAAGAAAATACCCAA 823

Qy       2384 AAATAGGATGGAAAGTTTTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAA 2443
```

```
                 || || ||||||     |  | || || | |  | |  || ||| ||  |    || ||
Db        824 GAAAAGAATGGAATAAAATTGAAAGAAAAATTGCGAAAAAAATGGGGACATATCGCAAAA 883

Qy       2444 CCAAACATAAAGAGTTAAATGCATGGTAGGCTC 2476
                |   || ||  | | || | || |  |  ||
Db        884 ATATTTATGAATGGATTAAAGAATTGGGGCTTC 916
```

Search completed: April 1, 2005, 14:50:22
Job time : 655 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:52:02 ; Search time 11110 Seconds
(without alignments)
11082.115 Million cell updates/sec

Title: US-10-751-612-1
Perfect score: 3016
Sequence: 1 tctagagcataggcattgta.....gggctatgtcaagtccatgg 3016

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US108A_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
86: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq:*
93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq:*
94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*

```
117:  /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
118:  /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
119:  /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
120:  /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
121:  /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
122:  /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
123:  /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
124:  /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
125:  /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
126:  /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
127:  /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
128:  /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
129:  /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3016	100.0	3016	2	PCT-US04-00113-1	Sequence 1, Appli
	2	3016	100.0	3016	62	US-10-751-612-1	Sequence 1, Appli
	3	120.8	4.0	576	54	US-10-425-115-151068	Sequence 151068,
	4	120.2	4.0	622	62	US-10-767-701-19690	Sequence 19690, A
c	5	118.6	3.9	3688	1	PCT-US99-05985-10	Sequence 10, Appl
c	6	118.6	3.9	3691	1	PCT-US99-05985-3	Sequence 3, Appli
c	7	118.6	3.9	5174	1	PCT-US99-05985-8	Sequence 8, Appli
c	8	100.8	3.3	1346	62	US-10-767-701-11451	Sequence 11451, A
c	9	96.4	3.2	398	36	US-09-850-147-6517	Sequence 6517, Ap
c	10	96.4	3.2	398	62	US-10-767-701-18110	Sequence 18110, A
c	11	96.4	3.2	398	89	US-60-202-213-6504	Sequence 6504, Ap
c	12	96.4	3.2	404	29	US-09-654-617-455751	Sequence 455751,
c	13	96.4	3.2	404	31	US-09-684-016-455751	Sequence 455751,
	14	89.4	3.0	1318	62	US-10-767-701-10015	Sequence 10015, A
	15	89.4	3.0	2032	54	US-10-425-115-42192	Sequence 42192, A
c	16	88	2.9	1894	50	US-10-219-999-16787	Sequence 16787, A
c	17	88	2.9	1894	54	US-10-425-114-32756	Sequence 32756, A
c	18	88	2.9	1894	54	US-10-425-114A-32756	Sequence 32756, A
c	19	88	2.9	1894	54	US-10-425-115-183742	Sequence 183742,
c	20	88	2.9	1934	37	US-09-865-439A-11469	Sequence 11469, A
c	21	86.8	2.9	803	37	US-09-861-478-1362	Sequence 1362, Ap
	22	86.2	2.9	255	20	US-09-304-517A-37239	Sequence 37239, A
	23	86.2	2.9	255	21	US-09-371-146A-37239	Sequence 37239, A
	24	86.2	2.9	255	45	US-09-985-678-37239	Sequence 37239, A
	25	86.2	2.9	271	20	US-09-304-517A-73374	Sequence 73374, A
	26	86.2	2.9	271	21	US-09-371-146A-73374	Sequence 73374, A
	27	86.2	2.9	271	45	US-09-985-678-73374	Sequence 73374, A
	28	86.2	2.9	274	20	US-09-304-517A-28685	Sequence 28685, A
	29	86.2	2.9	274	21	US-09-371-146A-28685	Sequence 28685, A
	30	86.2	2.9	274	45	US-09-985-678-28685	Sequence 28685, A
	31	86.2	2.9	296	19	US-09-266-640A-4305	Sequence 4305, Ap
	32	86.2	2.9	296	19	US-09-266-640B-4305	Sequence 4305, Ap
	33	86.2	2.9	296	37	US-09-863-524-4305	Sequence 4305, Ap
	34	86.2	2.9	297	20	US-09-304-517A-5449	Sequence 5449, Ap
	35	86.2	2.9	297	21	US-09-371-146A-5449	Sequence 5449, Ap
	36	86.2	2.9	297	45	US-09-985-678-5449	Sequence 5449, Ap
	37	86.2	2.9	304	20	US-09-304-517A-29762	Sequence 29762, A
	38	86.2	2.9	304	21	US-09-371-146A-29762	Sequence 29762, A
	39	86.2	2.9	304	45	US-09-985-678-29762	Sequence 29762, A
	40	86.2	2.9	310	20	US-09-304-517A-29797	Sequence 29797, A
	41	86.2	2.9	310	21	US-09-371-146A-29797	Sequence 29797, A
	42	86.2	2.9	310	45	US-09-985-678-29797	Sequence 29797, A
	43	86.2	2.9	337	27	US-09-617-682A-11847	Sequence 11847, A
	44	86.2	2.9	337	29	US-09-654-617-286972	Sequence 286972,
	45	86.2	2.9	337	31	US-09-684-016-286972	Sequence 286972,

ALIGNMENTS

```
RESULT 1
PCT-US04-00113-1
; Sequence 1, Application PC/TUS0400113
; GENERAL INFORMATION:
;  APPLICANT: The Texas A&M University System
;  TITLE OF INVENTION: STEM-REGULATED, PLANT DEFENSE PROMOTER
;  TITLE OF INVENTION:  AND USES THEREOF IN TISSUE-SPECIFIC EXPRESSION IN MONOCOTS
;  FILE REFERENCE: 017575.0893
;  CURRENT APPLICATION NUMBER: PCT/US04/00113
;  CURRENT FILING DATE:  2004-01-05
;  PRIOR APPLICATION NUMBER: 60/437,890
;  PRIOR FILING DATE: 2003-01-03
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3016
;   TYPE: DNA
;   ORGANISM: Sugarcane
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1)...(3012)
;   OTHER INFORMATION: o-methyltransferase promoter
;   FEATURE:
;   NAME/KEY: CAAT_signal
;   LOCATION: (2661)...(2664)
;   FEATURE:
;   NAME/KEY: TATA_signal
;   LOCATION: (2849)...(2855)
PCT-US04-00113-1

  Query Match           100.0%;  Score 3016;  DB 2;  Length 3016;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3016;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTAGAGCATAGGCATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTAGAGCATAGGCATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA 60

Qy         61 ACCTTAGGTATCCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCGGTCTGGTTGGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCTTAGGTATCCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCGGTCTGGTTGGAT 120

Qy        121 TTGTAGCGGGTTTCATGCAAAATAAGTTAGAAATCGTGCAAACTTGCAATGGAGGTTAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGTAGCGGGTTTCATGCAAAATAAGTTAGAAATCGTGCAAACTTGCAATGGAGGTTAAA 180

Qy        181 TTTGAAATATATTTGCATAGACAAAACAAATATAGATTATGAATGGTAATCCAATATGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTGAAATATATTTGCATAGACAAAACAAATATAGATTATGAATGGTAATCCAATATGAC 240

Qy        241 TTGCATTTTCTAACTCTATTGCTACTGTGCCAGATGAAGAATGTTGATCTGGAGAAGTTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGCATTTTCTAACTCTATTGCTACTGTGCCAGATGAAGAATGTTGATCTGGAGAAGTTT 300

Qy        301 TGTGAGAATGTGACAACAACGGGAGGTCATATCAAGATTCTGGGTACCCGCGGAGAATCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGAGAATGTGACAACAACGGGAGGTCATATCAAGATTCTGGGTACCCGCGGAGAATCG 360

Qy        361 GCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAATTGGCTGAGATGCCCCCATGTAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAATTGGCTGAGATGCCCCCATGTAG 420

Qy        421 TCGTCAGGCATGGAGAGTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCGTCAGGCATGGAGAGTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAG 480

Qy        481 AAGAATGCTAGTCTAATAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGAATGCTAGTCTAATAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCAT 540

Qy        541 TTTTCACATGCTAGCGCCTTTTGCCTGCTTTATTTAATTCAATTGGGTCCGATAAGCATG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTCACATGCTAGCGCCTTTTGCCTGCTTTATTTAATTCAATTGGGTCCGATAAGCATG 600
```

```
Qy       601 TGAACGTGGGAGACGGTTCCGTCGGACGGCTCCGTTTTCTTGTAGCGTACGGCGTGGACG 660
Db       601 TGAACGTGGGAGACGGTTCCGTCGGACGGCTCCGTTTTCTTGTAGCGTACGGCGTGGACG 660

Qy       661 GAGAAAAGGTGAGGGCCTATCTCTAAAGGGGAACGAATGGATGGTGGACACGTGTGGGGA 720
Db       661 GAGAAAAGGTGAGGGCCTATCTCTAAAGGGGAACGAATGGATGGTGGACACGTGTGGGGA 720

Qy       721 GACACCGAAGGGACATGCCGAGGAGGCACACAAGCTTCAGCAGGCGTCTCCAGACTCTCA 780
Db       721 GACACCGAAGGGACATGCCGAGGAGGCACACAAGCTTCAGCAGGCGTCTCCAGACTCTCA 780

Qy       781 GAAGAAGAAGAAGCTCACGGCACGGTTGCGGCTGGTTCTTGCTGTCGCTGTCTCGTGGTG 840
Db       781 GAAGAAGAAGAAGCTCACGGCACGGTTGCGGCTGGTTCTTGCTGTCGCTGTCTCGTGGTG 840

Qy       841 CACGTTTCTGTGATCACGCTGAAATCGACCGGCCGGCGGACCAACAGGAGGTCAGCTCGG 900
Db       841 CACGTTTCTGTGATCACGCTGAAATCGACCGGCCGGCGGACCAACAGGAGGTCAGCTCGG 900

Qy       901 CCACTCCGTCTCCGAGCGCATGAGTGCACCGTTCGTCCGCGGTTCCTTTTCTCGTGGTGC 960
Db       901 CCACTCCGTCTCCGAGCGCATGAGTGCACCGTTCGTCCGCGGTTCCTTTTCTCGTGGTGC 960

Qy       961 CGTGCACGCCTCTGCGTTCACCGGCACCCTGAAACCAATCAGAACGTTCCCTTTACAGGG 1020
Db       961 CGTGCACGCCTCTGCGTTCACCGGCACCCTGAAACCAATCAGAACGTTCCCTTTACAGGG 1020

Qy      1021 GAAAGGGACAAGTCTGATAACCTCTCTGTTTCCATCGTCCTCTAACCGCGAAGAGCGGAC 1080
Db      1021 GAAAGGGACAAGTCTGATAACCTCTCTGTTTCCATCGTCCTCTAACCGCGAAGAGCGGAC 1080

Qy      1081 GCACAAGACTTAGAGTCTATTTGTTCGAAATTTTTTACTCTCACAAAAGCTAGCTTTTAT 1140
Db      1081 GCACAAGACTTAGAGTCTATTTGTTCGAAATTTTTTACTCTCACAAAAGCTAGCTTTTAT 1140

Qy      1141 AGACGGGCATAAAAGCTATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATG 1200
Db      1141 AGACGGGCATAAAAGCTATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATG 1200

Qy      1201 AATATCATGTCGAACTATGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAA 1260
Db      1201 AATATCATGTCGAACTATGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAA 1260

Qy      1261 TTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGC 1320
Db      1261 TTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGC 1320

Qy      1321 TTGTGAGCTACTCCGCTCTACATTTAGTTGGTATCATAAATATTATTATATTATCATATA 1380
Db      1321 TTGTGAGCTACTCCGCTCTACATTTAGTTGGTATCATAAATATTATTATATTATCATATA 1380

Qy      1381 AATTTGATCAACTTGAGATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGG 1440
Db      1381 AATTTGATCAACTTGAGATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGG 1440

Qy      1441 GGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACAT 1500
Db      1441 GGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACAT 1500

Qy      1501 TAAATAAGCTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAG 1560
Db      1501 TAAATAAGCTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAG 1560

Qy      1561 TAGAGAGAGTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTG 1620
Db      1561 TAGAGAGAGTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTG 1620

Qy      1621 GTAAGAGGGCCATGAAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTA 1680
Db      1621 GTAAGAGGGCCATGAAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTA 1680

Qy      1681 TGTTTCAAAATCTGCATGCATGCATGCTTTGAATATTGTAACCTCACATTAACTCCCCTC 1740
Db      1681 TGTTTCAAAATCTGCATGCATGCATGCTTTGAATATTGTAACCTCACATTAACTCCCCTC 1740

Qy      1741 ACACATGCATGCAAACGGGCGGTGCACGCAAAAGAATTGAGTGAAGATGCACATGAAAAA 1800
Db      1741 ACACATGCATGCAAACGGGCGGTGCACGCAAAAGAATTGAGTGAAGATGCACATGAAAAA 1800

Qy      1801 TAAGTAAAATGCTTTGGCTTCATCACCCGGCTTAAATGCTCGACAGAAAAACACGTCGGT 1860
Db      1801 TAAGTAAAATGCTTTGGCTTCATCACCCGGCTTAAATGCTCGACAGAAAAACACGTCGGT 1860

Qy      1861 AGTCAAGGTTGTGCCTAACAAACTGGGGTTCACATGTAAAACACGTTCATGCCTTAGAAA 1920
Db      1861 AGTCAAGGTTGTGCCTAACAAACTGGGGTTCACATGTAAAACACGTTCATGCCTTAGAAA 1920

Qy      1921 CGGCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG 1980
Db      1921 CGGCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG 1980

Qy      1981 CTCTAAACTAGTTTTATGTGTCACGGTGGAGGAGAGGGAGGCTAAAAATATAATCTTGAG 2040
Db      1981 CTCTAAACTAGTTTTATGTGTCACGGTGGAGGAGAGGGAGGCTAAAAATATAATCTTGAG 2040

Qy      2041 CTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATACATGATAGATACAATATGA 2100
Db      2041 CTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATACATGATAGATACAATATGA 2100

Qy      2101 GAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCATACAATATGAGATTTCAT 2160
Db      2101 GAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCATACAATATGAGATTTCAT 2160

Qy      2161 CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT 2220
Db      2161 CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT 2220

Qy      2221 TAGTTGTTAGTAGTGTAAGACCTAGTTTAGTGCTCTTTTCTTGTCTAGGTTTATGTTGTG 2280
Db      2221 TAGTTGTTAGTAGTGTAAGACCTAGTTTAGTGCTCTTTTCTTGTCTAGGTTTATGTTGTG 2280

Qy      2281 TTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCATCTAATTCTAAAATGATGC 2340
Db      2281 TTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCATCTAATTCTAAAATGATGC 2340

Qy      2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTAAAATAGGATGGAAAGTT 2400
Db      2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTAAAATAGGATGGAAAGTT 2400

Qy      2401 TTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAACCAAACATAAAGAGTTA 2460
Db      2401 TTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAACCAAACATAAAGAGTTA 2460

Qy      2461 AATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAAACTCTCAAA 2520
Db      2461 AATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAAACTCTCAAA 2520

Qy      2521 TTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTAGATCTACAAACTCTCAAA 2580
Db      2521 TTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTAGATCTACAAACTCTCAAA 2580

Qy      2581 ATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTAGGCAAGAAAAGTTAGATA 2640
Db      2581 ATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTAGGCAAGAAAAGTTAGATA 2640

Qy      2641 ATTTTGATAAGCTATGGGACCAAATTAATTTATGTATGCATGCTCGAACTAGTTGATGAT 2700
Db      2641 ATTTTGATAAGCTATGGGACCAAATTAATTTATGTATGCATGCTCGAACTAGTTGATGAT 2700

Qy      2701 GATGGACCCCATAATAGACACTAGTTCATGGGCTGGTTTCCTTGTATAGTACTAGCTAGT 2760
Db      2701 GATGGACCCCATAATAGACACTAGTTCATGGGCTGGTTTCCTTGTATAGTACTAGCTAGT 2760

Qy      2761 ATAACTTTTTCAAGTTGTAGCTACTACTTTAGCTTATACTCCGCATATTACAATCAAATA 2820
```

```
Db       2761 ATAACTTTTTCAAGTTGTAGCTACTACTTTAGCTTATACTCCGCATATTACAATCAAATA 2820

Qy       2821 GAATTCGGAAGTACTATAAACGGGAGCCTATAAATGGAGACGTTTTGCATCATGAGGCTA 2880

Db       2821 GAATTCGGAAGTACTATAAACGGGAGCCTATAAATGGAGACGTTTTGCATCATGAGGCTA 2880

Qy       2881 TAACAACTTGAGCAAAAACAGAAGCCGTGCGCCATGGCGCTCAGCAAGGAGCAACACACA 2940

Db       2881 TAACAACTTGAGCAAAAACAGAAGCCGTGCGCCATGGCGCTCAGCAAGGAGCAACACACA 2940

Qy       2941 AGCACTGATCAGCAGGCCGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACCCTGGGC 3000

Db       2941 AGCACTGATCAGCAGGCCGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACCCTGGGC 3000

Qy       3001 TATGTCAAGTCCATGG 3016

Db       3001 TATGTCAAGTCCATGG 3016
```

RESULT 2
US-10-751-612-1
; Sequence 1, Application US/10751612
; GENERAL INFORMATION:
; APPLICANT: Mirkov, T. Erik
; APPLICANT: Damaj, Mona B.,
; APPLICANT: Reddy, Avutu,
; APPLICANT: Thomas, Terry L.,
; APPLICANT: Rathore, Keerti S.,
; APPLICANT: Emani, Chandrakanth,
; APPLICANT: Kumpatla, Siva Prasad
; TITLE OF INVENTION: STEM-REGULATED, PLANT DEFENSE PROMOTER
; TITLE OF INVENTION: AND USES THEREOF IN TISSUE-SPECIFIC EXPRESSION IN MONOCOTS
; FILE REFERENCE: 017575.0774
; CURRENT APPLICATION NUMBER: US/10/751,612
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: 60/437,890
; PRIOR FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3016
; TYPE: DNA
; ORGANISM: Sugarcane
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(3012)
; OTHER INFORMATION: o-methyltransferase promoter
; FEATURE:
; NAME/KEY: CAAT_signal
; LOCATION: (2661)...(2664)
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: (2849)...(2855)
US-10-751-612-1

Query Match 100.0%; Score 3016; DB 62; Length 3016;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCTAGAGCATAGGCATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA 60

Db          1 TCTAGAGCATAGGCATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA 60

Qy         61 ACCTTAGGTATCCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCGGTCTGGTTGGAT 120

Db         61 ACCTTAGGTATCCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCGGTCTGGTTGGAT 120

Qy        121 TTGTAGCGGGTTTCATGCAAAATAAGTTAGAAATCGTGCAAACTTGCAATGGAGGTTAAA 180

Db        121 TTGTAGCGGGTTTCATGCAAAATAAGTTAGAAATCGTGCAAACTTGCAATGGAGGTTAAA 180

Qy        181 TTTGAAATATATTTGCATAGACAAAACAAATATAGATTATGAATGGTAATCCAATATGAC 240

Db        181 TTTGAAATATATTTGCATAGACAAAACAAATATAGATTATGAATGGTAATCCAATATGAC 240

Qy        241 TTGCATTTTCTAACTCTATTGCTACTGTGCCAGATGAAGAATGTTGATCTGGAGAAGTTT 300

Db        241 TTGCATTTTCTAACTCTATTGCTACTGTGCCAGATGAAGAATGTTGATCTGGAGAAGTTT 300

Qy        301 TGTGAGAATGTGACAACAACGGGAGGTCATATCAAGATTCTGGGTACCCGCGGAGAATCG 360

Db        301 TGTGAGAATGTGACAACAACGGGAGGTCATATCAAGATTCTGGGTACCCGCGGAGAATCG 360

Qy        361 GCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAATTGGCTGAGATGCCCCCATGTAG 420

Db        361 GCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAATTGGCTGAGATGCCCCCATGTAG 420

Qy        421 TCGTCAGGCATGGAGAGTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAG 480

Db        421 TCGTCAGGCATGGAGAGTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAG 480

Qy        481 AAGAATGCTAGTCTAATAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCAT 540

Db        481 AAGAATGCTAGTCTAATAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCAT 540

Qy        541 TTTTCACATGCTAGCGCCTTTTGCCTGCTTTATTTAATTCAATTGGGTCCGATAAGCATG 600

Db        541 TTTTCACATGCTAGCGCCTTTTGCCTGCTTTATTTAATTCAATTGGGTCCGATAAGCATG 600

Qy        601 TGAACGTGGGAGACGGTTCCGTCGGACGGCTCCGTTTTCTTGTAGCGTACGGCGTGGACG 660

Db        601 TGAACGTGGGAGACGGTTCCGTCGGACGGCTCCGTTTTCTTGTAGCGTACGGCGTGGACG 660

Qy        661 GAGAAAAGGTGAGGGCCTATCTCTAAAGGGGAACGAATGGATGGTGGACACGTGTGGGGA 720

Db        661 GAGAAAAGGTGAGGGCCTATCTCTAAAGGGGAACGAATGGATGGTGGACACGTGTGGGGA 720

Qy        721 GACACCGAAGGGACATGCCGAGGAGGCACACAAGCTTCAGCAGGCGTCTCCAGACTCTCA 780

Db        721 GACACCGAAGGGACATGCCGAGGAGGCACACAAGCTTCAGCAGGCGTCTCCAGACTCTCA 780

Qy        781 GAAGAAGAAGAAGCTCACGGCACGGTTGCGGCTGGTTCTTGCTGTCGCTGTCTCGTGGTG 840

Db        781 GAAGAAGAAGAAGCTCACGGCACGGTTGCGGCTGGTTCTTGCTGTCGCTGTCTCGTGGTG 840

Qy        841 CACGTTTCTGTGATCACGCTGAAATCGACCGGCCGGCGGACCAACAGGAGGTCAGCTCGG 900

Db        841 CACGTTTCTGTGATCACGCTGAAATCGACCGGCCGGCGGACCAACAGGAGGTCAGCTCGG 900

Qy        901 CCACTCCGTCTCCGAGCGCATGAGTGCACCGTTCGTCCGCGGTTCCTTTTCTCGTGGTGC 960

Db        901 CCACTCCGTCTCCGAGCGCATGAGTGCACCGTTCGTCCGCGGTTCCTTTTCTCGTGGTGC 960

Qy        961 CGTGCACGCCTCTGCGTTCACCGGCACCCTGAAACCAATCAGAACGTTCCCTTTACAGGG 1020

Db        961 CGTGCACGCCTCTGCGTTCACCGGCACCCTGAAACCAATCAGAACGTTCCCTTTACAGGG 1020

Qy       1021 GAAAGGGACAAGTCTGATAACCTCTCTGTTTCCATCGTCCTCTAACCGCGAAGAGCGGAC 1080

Db       1021 GAAAGGGACAAGTCTGATAACCTCTCTGTTTCCATCGTCCTCTAACCGCGAAGAGCGGAC 1080

Qy       1081 GCACAAGACTTAGAGTCTATTTGTTCGAAATTTTTTACTCTCACAAAAGCTAGCTTTTAT 1140

Db       1081 GCACAAGACTTAGAGTCTATTTGTTCGAAATTTTTTACTCTCACAAAAGCTAGCTTTTAT 1140

Qy       1141 AGACGGGCATAAAAGCTATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATG 1200

Db       1141 AGACGGGCATAAAAGCTATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATG 1200

Qy       1201 AATATCATGTCGAACTATGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAA 1260

Db       1201 AATATCATGTCGAACTATGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAA 1260

Qy       1261 TTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGC 1320
```

```
Db      1261 TTGTACTTTTAGTTGTTTGAGCATGAAGGTCTGAACTATGAATTTATGATGTATTGTGGC 1320
Qy      1321 TTGTGAGCTACTCCGCTCTACATTTAGTTGGTATCATAAATATTATTATATTATCATATA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TTGTGAGCTACTCCGCTCTACATTTAGTTGGTATCATAAATATTATTATATTATCATATA 1380
Qy      1381 AATTTGATCAACTTGAGATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 AATTTGATCAACTTGAGATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGG 1440
Qy      1441 GGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 GGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACAT 1500
Qy      1501 TAAATAAGCTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TAAATAAGCTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAG 1560
Qy      1561 TAGAGAGAGTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TAGAGAGAGTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTG 1620
Qy      1621 GTAAGAGGGCCATGAAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 GTAAGAGGGCCATGAAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTA 1680
Qy      1681 TGTTTCAAAATCTGCATGCATGCATGCTTTGAATATTGTAACCTCACATTAACTCCCCTC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 TGTTTCAAAATCTGCATGCATGCATGCTTTGAATATTGTAACCTCACATTAACTCCCCTC 1740
Qy      1741 ACACATGCATGCAAACGGGCGGTGCACGCAAAAGAATTGAGTGAAGATGCACATGAAAAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 ACACATGCATGCAAACGGGCGGTGCACGCAAAAGAATTGAGTGAAGATGCACATGAAAAA 1800
Qy      1801 TAAGTAAAATGCTTTGGCTTCATCACCCGGCTTAAATGCTCGACAGAAAAACACGTCGGT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TAAGTAAAATGCTTTGGCTTCATCACCCGGCTTAAATGCTCGACAGAAAAACACGTCGGT 1860
Qy      1861 AGTCAAGGTTGTGCCTAACAAACTGGGGTTCACATGTAAAACACGTTCATGCCTTAGAAA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 AGTCAAGGTTGTGCCTAACAAACTGGGGTTCACATGTAAAACACGTTCATGCCTTAGAAA 1920
Qy      1921 CGGCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 CGGCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG 1980
Qy      1981 CTCTAAACTAGTTTTATGTGTCACGGTGGAGGAGAGGGAGGCTAAAAATATAATCTTGAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 CTCTAAACTAGTTTTATGTGTCACGGTGGAGGAGAGGGAGGCTAAAAATATAATCTTGAG 2040
Qy      2041 CTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATACATGATAGATACAATATGA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 CTAACGTGAAGAGAAGAGCTATTTTTTTTTGCTCCCCAATACATGATAGATACAATATGA 2100
Qy      2101 GAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCATACAATATGAGATTTCAT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GAGAAAAAATATATGAATAAAGAACACTTTACATGCCAGCCATACAATATGAGATTTCAT 2160
Qy      2161 CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT 2220
Qy      2221 TAGTTGTTAGTAGTGTAAGACCTAGTTTAGTGCTCTTTTCTTGTCTAGGTTTATGTTGTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 TAGTTGTTAGTAGTGTAAGACCTAGTTTAGTGCTCTTTTCTTGTCTAGGTTTATGTTGTG 2280
Qy      2281 TTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCATCTAATTCTAAAATGATGC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 TTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCATCTAATTCTAAAATGATGC 2340
Qy      2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTAAAATAGGATGGAAAGTT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCTAAAATAGGATGGAAAGTT 2400
```

```
Qy      2401 TTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAACCAAACATAAAGAGTTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TTGTAGAGTAATAATTGGTATGAAGTGGCGAAGTCGACCACAACCAAACATAAAGAGTTA 2460
Qy      2461 AATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAAACTCTCAAA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 AATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAAACTCTCAAA 2520
Qy      2521 TTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTAGATCTACAAACTCTCAAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 TTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTAGATCTACAAACTCTCAAA 2580
Qy      2581 ATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTAGGCAAGAAAAGTTAGATA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 ATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTAGGCAAGAAAAGTTAGATA 2640
Qy      2641 ATTTTGATAAGCTATGGGACCAAATTAATTTATGTATGCATGCTCGAACTAGTTGATGAT 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 ATTTTGATAAGCTATGGGACCAAATTAATTTATGTATGCATGCTCGAACTAGTTGATGAT 2700
Qy      2701 GATGGACCCCATAATAGACACTAGTTCATGGGCTGGTTTCCTTGTATAGTACTAGCTAGT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 GATGGACCCCATAATAGACACTAGTTCATGGGCTGGTTTCCTTGTATAGTACTAGCTAGT 2760
Qy      2761 ATAACTTTTTCAAGTTGTAGCTACTACTTTAGCTTATACTCCGCATATTACAATCAAATA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 ATAACTTTTTCAAGTTGTAGCTACTACTTTAGCTTATACTCCGCATATTACAATCAAATA 2820
Qy      2821 GAATTCGGAAGTACTATAAACGGGAGCCTATAAATGGAGACGTTTTGCATCATGAGGCTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 GAATTCGGAAGTACTATAAACGGGAGCCTATAAATGGAGACGTTTTGCATCATGAGGCTA 2880
Qy      2881 TAACAACTTGAGCAAAAACAGAAGCCGTGCGCCATGGCGCTCAGCAAGGAGCAACACACA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 TAACAACTTGAGCAAAAACAGAAGCCGTGCGCCATGGCGCTCAGCAAGGAGCAACACACA 2940
Qy      2941 AGCACTGATCAGCAGGCCGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACCCTGGGC 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 AGCACTGATCAGCAGGCCGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACCCTGGGC 3000
Qy      3001 TATGTCAAGTCCATGG 3016
             ||||||||||||||||
Db      3001 TATGTCAAGTCCATGG 3016
```

RESULT 3
US-10-425-115-151068
; Sequence 151068, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 151068
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_69292C.1
US-10-425-115-151068

Query Match 4.0%; Score 120.8; DB 54; Length 576;
Best Local Similarity 66.9%; Pred. No. 3.3e-20;
Matches 198; Conservative 0; Mismatches 77; Indels 21; Gaps 1;

```
Qy       278 AGAATGTTGATCTGGAGAAGTTTTGTGAGAATGTGACAACAACGGGAGGTCATATCAAGA 337
```

```
           |||||||||||||  | | ||| | |||| ||| |||||||||  ||||  |||||||||
Db        281 AGAATGTTGATCTACATAGGTTCTATGAGGATGCGACAACAACACGAGGCTATATCAAGA 340

Qy        338 TTCTGGGTACCCGCGGAGAATCGGCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAA 397
             |||||||||  | |||||||||  | |||||||  ||| ||||||||||||||||||||||
Db        341 CTCTGGGTACATGAGGAGAATCGTCTTCCATGTGGTTTGCCTCGTCAGGCATGGGGGGAA 400

Qy        398 TTGGCTGAGATGCCCCCATGTA--------------------GTCGTCAGGCATGGAGA 436
             ||||||||||||||||  | ||                    ||||||||||||||||
Db        401 TTGGCTGAGATGCCCCCGTATAGCTGGTCTTGTTGGCACTGGTGTCGTCAGGCATGGAGA 460

Qy        437 GTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAGAAGAATGCTAGTCTAA 496
             | | ||| ||||||               |    ||  |  |    ||  |  ||    ||
Db        461 GAATTGGGTGAGATTGAGAGAAACGAGAAGAAGAATGCTAATCTAATTACCCTTCCGTAT 520

Qy        497 TAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCATTTTTCACATGCT 552
               | |   |     |     |||||||||||||||| || ||||||||||| |||
Db        521 CTAGATGATAATTTGATGGAACCAACTATTATAATTAGCGCCATTTTTCACAGGCT 576


RESULT 4
US-10-767-701-19690
; Sequence 19690, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 19690
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB5047-010-R1-XP1-B5
US-10-767-701-19690

  Query Match             4.0%;  Score 120.2;  DB 62;  Length 622;
  Best Local Similarity   66.7%;  Pred. No. 5e-20;
  Matches  198;  Conservative    0;  Mismatches   78;  Indels   21;  Gaps    1;

Qy        278 AGAATGTTGATCTGGAGAAGTTTTGTGAGAATGTGACAACAACGGGAGGTCATATCAAGA 337
             |||||||||||||  | | ||| | |||| ||| |||||||||  ||||  |||||||||
Db        304 AGAATGTTGATCTACATAGGTTCTATGAGGATGCGACAACAACACGAGGCTATATCAAGA 363

Qy        338 TTCTGGGTACCCGCGGAGAATCGGCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAA 397
             |||||||||  | |||||||||  | |||||||  ||| ||||||||||||||||||||||
Db        364 CTCTGGGTACATGAGGAGAATCGTCTTCCATGTGGTTTGCCTCGTCAGGCATGGGGGGAA 423

Qy        398 TTGGCTGAGATGCCCCCATGTA--------------------GTCGTCAGGCATGGAGA 436
             ||||||||||||||||  | ||                    ||||||||||||||||
Db        424 TTGGCTGAGATGCCCCCGTATAGCTGGTCTTGTTGGCACTGGTGTCGTCAGGCATGGAGA 483

Qy        437 GTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAGAAGAATGCTAGTCTAA 496
             | | ||| ||||||               |    ||  |  |    ||  |  ||    ||
Db        484 GAATTGGGTGAGATTGAGAGAAACGAGAAGAAGAATGCTAATCTAATTACCCTTCCGTAT 543

Qy        497 TAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCATTTTTCACATGCTA 553
               | |   |     |||||||||||||||| || ||||||||||| || |
Db        544 CTAGATGATAATTTGATGGAACCAACTATTATAATTAGCGCCATTTTTCACAGGCAA 600


RESULT 5
PCT-US99-05985-10/c
; Sequence 10, Application PC/TUS9905985A
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT: Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-03648
;  CURRENT APPLICATION NUMBER: PCT/US99/05985A
;  CURRENT FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 3688
;   TYPE: DNA
;   ORGANISM: Saccharum Hybrid Cultivar 32-8560
PCT-US99-05985-10

  Query Match             3.9%;  Score 118.6;  DB 1;  Length 3688;
  Best Local Similarity   86.0%;  Pred. No. 3.1e-19;
  Matches  166;  Conservative    0;  Mismatches   24;  Indels    3;  Gaps    3;

Qy       1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT 1510
              || ||||| ||||| ||||||||| || ||||||||||||||||||||||||||||| |||
Db       1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT 1856

Qy       1511 GATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGT 1570
              |||||| |||||||||||||||||||||||||||||||||||||  | ||||||||||
Db       1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGAGT 1796

Qy       1571 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
              || | |  |||||||||||| || |||||||| | ||||||  | ||||||  ||| | |
Db       1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736

Qy       1629 GCCATGAAATCTC 1641
              ||||| ||||| |
Db       1735 GCCATAAAATCCC 1723


RESULT 6
PCT-US99-05985-3/c
; Sequence 3, Application PC/TUS9905985A
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT: Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-03648
;  CURRENT APPLICATION NUMBER: PCT/US99/05985A
;  CURRENT FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 3691
;   TYPE: DNA
;   ORGANISM: Saccharum Hybrid Cultivar H32-8560
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (9)
;   OTHER INFORMATION: The residue in this position could be any
;   OTHER INFORMATION: nucleotide.
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3613)
;   OTHER INFORMATION: The residue in this position could be any
;   OTHER INFORMATION: nucleotide.
PCT-US99-05985-3

  Query Match             3.9%;  Score 118.6;  DB 1;  Length 3691;
  Best Local Similarity   86.0%;  Pred. No. 3.1e-19;
  Matches  166;  Conservative    0;  Mismatches   24;  Indels    3;  Gaps    3;

Qy       1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT 1510
              || ||||| ||||| ||||||||| || ||||||||||||||||||||||||||||| |||
Db       1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT 1856

Qy       1511 GATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGT 1570
              |||||| |||||||||||||||||||||||||||||||||||||  | ||||||||||
Db       1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGAGT 1796

Qy       1571 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
```

```
                ||  |  |  |||||||||||||  || ||||||||  |  |||||  |  ||||||  |||  |  |
Db       1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736

Qy       1629 GCCATGAAATCTC 1641
                |||||  |||||  |
Db       1735 GCCATAAAATCCC 1723


RESULT 7
PCT-US99-05985-8/c
; Sequence 8, Application PC/TUS9905985A
; GENERAL INFORMATION:
;  APPLICANT: Albert, Henrik H.
;  APPLICANT: Wei, Hairong
;  TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
;  FILE REFERENCE: UH-03648
;  CURRENT APPLICATION NUMBER: PCT/US99/05985A
;  CURRENT FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 5174
;   TYPE: DNA
;   ORGANISM: Saccharum Hybrid Cultivar H32-8560
PCT-US99-05985-8

  Query Match             3.9%;  Score 118.6;  DB 1;  Length 5174;
  Best Local Similarity   86.0%;  Pred. No. 3.7e-19;
  Matches  166;  Conservative    0;  Mismatches   24;  Indels    3;  Gaps    3;

Qy       1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT 1510
                ||  ||||||  |||||  ||||||||  ||  ||||||||||||||||||||||||||  |||
Db       1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT 1856

Qy       1511 GATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGT 1570
                ||||||  |||||||||||||||||||||||||||||||||||||||  |  ||||||||||
Db       1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGAGT 1796

Qy       1571 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                ||  |  |  |||||||||||  ||  ||||||||  |  ||||||  |  ||||||  |||  |  |
Db       1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736

Qy       1629 GCCATGAAATCTC 1641
                |||||  |||||  |
Db       1735 GCCATAAAATCCC 1723


RESULT 8
US-10-767-701-11451/c
; Sequence 11451, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11451
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3954_1
US-10-767-701-11451

  Query Match             3.3%;  Score 100.8;  DB 62;  Length 1346;
  Best Local Similarity   70.2%;  Pred. No. 9.4e-15;
  Matches  160;  Conservative    0;  Mismatches   47;  Indels   21;  Gaps    1;

Qy       1455 TTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATG 1514
                |  ||||||||||  ||||  |||  |||||||  ||||||||||  ||||||||||  |||||||
Db       1291 TACTAAGGCCAGGCTCAATGGAGTTTCATGAGAGTTTCATGCACATTAAATATGCTGATG 1232

Qy       1515 TGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGTTTCA 1574
                ||  |  |  ||  |  ||||||||||||||||||||||||||||  ||  |
Db       1231 TGGCGCTATAGTAATGAAGAGAGAGATGATAAGAGTTTTATCC---------------- 1189

Qy       1575 TGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGGCCATG 1634
                ||||||||||  |  ||||||||||||||||  |||||  |||  ||  ||||  |||
Db       1188 ----CATGAAACTCTAATGCACTGTTTCCAAAATACAGATGTGTTGAAAACTGGGCTATG 1133

Qy       1635 AAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTATG 1682
                |||   |  |  |||   ||  |||||||  |||  ||    |  ||    |||
Db       1132 AAACTGCCATTGAGGATGGCCTAAGAGGAGGTTTCTACGAGATTAATG 1085


RESULT 9
US-09-850-147-6517/c
; Sequence 6517, Application US/09850147
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Scott E.
;  APPLICANT:  Edgerton, Michael D
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(51914)B
;  CURRENT APPLICATION NUMBER: US/09/850,147
;  CURRENT FILING DATE:  2001-05-08
;  PRIOR APPLICATION NUMBER: US 60/202,213
;  PRIOR FILING DATE: 2000-05-08
;  PRIOR APPLICATION NUMBER: US 09/654,617
;  PRIOR FILING DATE: 2000-09-05
;  PRIOR APPLICATION NUMBER: US 09/684,016
;  PRIOR FILING DATE: 2000-10-10
;  NUMBER OF SEQ ID NOS: 18014
; SEQ ID NO 6517
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   OTHER INFORMATION: Clone ID: LIB3478-007-P1-K1-B12
US-09-850-147-6517

  Query Match             3.2%;  Score 96.4;  DB 36;  Length 398;
  Best Local Similarity   79.4%;  Pred. No. 7.5e-14;
  Matches  127;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1449 GTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAG 1508
                |  |||   |  |||      | |  ||      | |||   |||||||||  ||||||||| |
Db        158 GGAGGCATACAAGTGTCCTGTTAGGCCACTCTCAATGGAGTTTCATTAACATTAAATATG 99

Qy       1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGA 1568
                ||||  ||  |||||||||  |||||||||||||||||||||||||||||  |||||||||
Db         98 CTGA--TGGCACCGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGAGA 41

Qy       1569 GTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAAT 1608
                ||||  ||||||||||||||||||  ||||  ||||||||||
Db         40 GTTTTATGGGGATGAAACTCTTCTGCACTATTTCCAAAAT 1


RESULT 10
US-10-767-701-18110/c
; Sequence 18110, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 18110
;   LENGTH: 398
```

```
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3478-007-P1-K1-B12
US-10-767-701-18110

  Query Match             3.2%;  Score 96.4;  DB 62;  Length 398;
  Best Local Similarity   79.4%;  Pred. No. 7.5e-14;
  Matches  127;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1449 GTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAG 1508
              | |||  |  |||     | | ||     | |||   |||||||||  |||||||||| |
Db        158 GGAGGCATACAAGTGTCCTGTTAGGCCACTCTCAATGGAGTTTCATTAACATTAAATATG 99

Qy       1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGA 1568
              ||||  || |||||||||| ||||||||||||||||||||||||||||||  ||||||||||
Db         98 CTGA--TGGCACCGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGAGA 41

Qy       1569 GTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAAT 1608
              |||| ||||||||||||||||||| |||| ||||||||||
Db          40 GTTTTATGGGGATGAAACTCTTCTGCACTATTTCCAAAAT 1


RESULT 11
US-60-202-213-6504/c
; Sequence 6504, Application US/60202213
; GENERAL INFORMATION:
;  APPLICANT:       Andersen, Scott E.
;  APPLICANT:  Edgerton, Michael D
;  TITLE OF INVENTION:       NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION:  PLANTS
;  FILE REFERENCE:       38-21(51914)A
;  CURRENT APPLICATION NUMBER: US/60/202,213
;  CURRENT FILING DATE:  2000-05-08
;  NUMBER OF SEQ ID NOS:       17986
; SEQ ID NO 6504
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   OTHER INFORMATION: Clone ID: LIB3478-007-P1-K1-B12
US-60-202-213-6504

  Query Match             3.2%;  Score 96.4;  DB 89;  Length 398;
  Best Local Similarity   79.4%;  Pred. No. 7.5e-14;
  Matches  127;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1449 GTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAG 1508
              | |||  |  |||     | | ||     | |||   |||||||||  |||||||||| |
Db        158 GGAGGCATACAAGTGTCCTGTTAGGCCACTCTCAATGGAGTTTCATTAACATTAAATATG 99

Qy       1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGA 1568
              ||||  || |||||||||| ||||||||||||||||||||||||||||||  ||||||||||
Db         98 CTGA--TGGCACCGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGAGA 41

Qy       1569 GTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAAT 1608
              |||| ||||||||||||||||||| |||| ||||||||||
Db          40 GTTTTATGGGGATGAAACTCTTCTGCACTATTTCCAAAAT 1


RESULT 12
US-09-654-617-455751/c
; Sequence 455751, Application US/09654617
; GENERAL INFORMATION:
;  APPLICANT:       Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)D
;  CURRENT APPLICATION NUMBER: US/09/654,617
;  CURRENT FILING DATE:  2000-09-05
;  NUMBER OF SEQ ID NOS:       463173
; SEQ ID NO 455751
;   LENGTH: 404
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
US-09-654-617-455751

  Query Match             3.2%;  Score 96.4;  DB 29;  Length 404;
  Best Local Similarity   79.4%;  Pred. No. 7.5e-14;
  Matches  127;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1449 GTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAG 1508
              | |||  |  |||     | | ||     | |||   |||||||||  |||||||||| |
Db        164 GGAGGCATACAAGTGTCCTGTTAGGCCACTCTCAATGGAGTTTCATTAACATTAAATATG 105

Qy       1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGA 1568
              ||||  || |||||||||| ||||||||||||||||||||||||||||||  ||||||||||
Db        104 CTGA--TGGCACCGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGAGA 47

Qy       1569 GTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAAT 1608
              |||| ||||||||||||||||||| |||| ||||||||||
Db         46 GTTTTATGGGGATGAAACTCTTCTGCACTATTTCCAAAAT 7


RESULT 13
US-09-684-016-455751/c
; Sequence 455751, Application US/09684016
; GENERAL INFORMATION:
;  APPLICANT:       Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  TITLE OF INVENTION:       Annotated Plant Genes
;  FILE REFERENCE:       38-21(15097)D
;  CURRENT APPLICATION NUMBER: US/09/684,016
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER:       US 09/654,617
;  PRIOR FILING DATE:       2000-09-05
;  NUMBER OF SEQ ID NOS:       463173
; SEQ ID NO 455751
;   LENGTH: 404
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
US-09-684-016-455751

  Query Match             3.2%;  Score 96.4;  DB 31;  Length 404;
  Best Local Similarity   79.4%;  Pred. No. 7.5e-14;
  Matches  127;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1449 GTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAG 1508
              | |||  |  |||     | | ||     | |||   |||||||||  |||||||||| |
Db        164 GGAGGCATACAAGTGTCCTGTTAGGCCACTCTCAATGGAGTTTCATTAACATTAAATATG 105

Qy       1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGA 1568
              ||||  || |||||||||| ||||||||||||||||||||||||||||||  ||||||||||
Db        104 CTGA--TGGCACCGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGAGA 47

Qy       1569 GTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCAAAAT 1608
              |||| ||||||||||||||||||| |||| ||||||||||
Db         46 GTTTTATGGGGATGAAACTCTTCTGCACTATTTCCAAAAT 7


RESULT 14
US-10-767-701-10015
; Sequence 10015, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 10015
;   LENGTH: 1318
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
```

```
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS4887_1
US-10-767-701-10015

  Query Match             3.0%;  Score 89.4;  DB 62;  Length 1318;
  Best Local Similarity   80.2%;  Pred. No. 9.4e-12;
  Matches  105;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1456 TCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGT 1515
             ||| || || |||||| ||| ||||||| | | ||||||| |||||||||| | | ||||
Db       1188 TCTTAGACCGGTCTCAATGGAGTTTCATTAAAATTTCATGCACATTAAATATGTTAATGT 1247

Qy       1516 GACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGTTTCAT 1575
               ||  ||||| ||||||||||||||||||||||||||||  || ||||||||||| ||
Db       1248 TGCATTGTATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGCAGAGAGAGTTTTAT 1307

Qy       1576 GGGGATGAAAC 1586
                 || ||||
Db       1308 CATCATAAAAC 1318


RESULT 15
US-10-425-115-42192
; Sequence 42192, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 42192
;   LENGTH: 2032
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_138478C.1
US-10-425-115-42192

  Query Match             3.0%;  Score 89.4;  DB 54;  Length 2032;
  Best Local Similarity   68.9%;  Pred. No. 1.2e-11;
  Matches  151;  Conservative    0;  Mismatches   66;  Indels    2;  Gaps    2;

Qy       1457 CTAAGGCCAGTCTCAGTGG-GGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGT 1515
             ||||| | |||||| |||| |||||||  ||||  | |||| ||||||||| | ||||||
Db        498 CTAAGACTAGTCTCTGTGGTGGTTTCACGAGAGGATTATGGGCATTAAATATGTTGATGT 557

Qy       1516 GACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGTTTCAT 1575
             | ||   |||| | |||||||||| | | ||| |  ||    ||| |  |  ||||| ||
Db        558 GGCATATTATTAACGAAGAGAGATAAGGTAAAAAGTTTTATCGAATGAAATGAGTTCCAC 617

Qy       1576 GGG-GATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGGCCATG 1634
             ||| |||||||||  | | ||||| ||| || |||| |  |  |||| || |  | |||
Db        618 GGGCGATGAAACTTATGTGCACTGCTTCTAACATATCGGAGTCTTGGGAACATTGACATA 677

Qy       1635 AAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCT 1673
             ||||| | | ||| |||| ||||| |     |  | |||
Db        678 AAATCCCCACTGAAACTGGCCTAATAAATAAGCTAATCT 716


Search completed: April  1, 2005, 17:55:43
Job time : 11115 secs
```